In the Specification

Please amend paragraph [0039] as follows:

[0039] If the number of sequences to analyze is larger, e.g., greater than 100, the alignment proposed by Clustal W. is too long and it is necessary to employ an iterative alignment based on a hidden Markov model, referred to below as HMM (Sean Eddy, "Hidden Markov Models", Curr. Opin. Struct. Biol. Vol. 6, pages 361-365, ~~1966~~ 1996).